IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Sherry Leonard *et al.*

Serial No.: 08/956,518   Group No.: 1645
Filed: 10/23/97   Examiner: R. Hayes
Entitled: **ALPHA-7 NICOTINIC RECEPTOR**

CERTIFICATE RE: SEQUENCE LISTING

Assistant Commissioner for Patents
Washington, D.C. 20231

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231.

Dated: *April 1, 1999*   By: *Marlene E. Garitano*
Marlene E. Garitano

Sir or Madam:

I hereby state that the enclosed Sequence Listing is being submitted in paper copy and on a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

The Commissioner is hereby authorized to charge any additional fee or credit overpayment to our Deposit Account No. 08-1290. **An originally executed duplicate of this Certificate is enclosed for this purpose.**

Dated: _1 April 1999_   By: *Kamrin MacKnight*
Kamrin T. MacKnight
Registration No. 38,230

MEDLEN & CARROLL, LLP
220 Montgomery Street, Suite 2200
San Francisco, California 94104
415.705.8410

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

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Washington, D.C. 20231

DN

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
08/956,518	10/23/97	LEONARD S	UTC-03042

HM12/0323

```
KAMRIN T. MACKNIGHT
MEDLEN & CARROLL
220 MONTGOMERY STREET
SUITE 2200
SAN FRANCISCO CA 94104
```

EXAMINER
HAYES, R

ART UNIT	PAPER NUMBER
1645	7

DATE MAILED: 03/23/99

Resp. 4/23/99 RLD

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

PTO-90C (Rev. 2/95)

U.S. GPO: 1999

UNITED ᴸ ⬤ ᴇS DEPARTMENT OF COMMERCE
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COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
08/956518			

EXAMINER	
ART UNIT	PAPER NUMBER
	7

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication filed on **01/07/99** is not fully responsive to the communication mailed **09/04/98** for the reason(s) set forth on the attached Notice to Comply With the Sequence Rules or CRF Diskette Problem Report. It should also be noted that 37 CFR 1.821 (a)(2)(c-d) states that each sequence disclosed must appear separately in the "Sequence listing" *and* in the text of the description and claims (i.e., where first mentioned in the specification). See MPEP 2431.

Since the response appears to be **bona fide**, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **Robert C. Hayes**, Art Unit **1645**, whose telephone number is **703-305-3132**

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

Robert C. Hayes, Ph.D.
March 19, 1999

ANTHONY C. CAPUTA
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
    Technical Assistance..703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RAW SEQUENCE LISTING
ERROR REPORT

MAY 1 3 2002
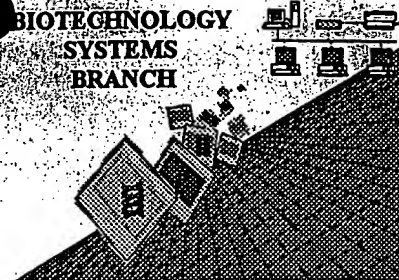
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _08/956,578_

Art Unit / Team No. : _1648_

Date Processed by STIC: _1/21/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 08/956,578 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

_____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation

Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of N's or Xaa's (NEW RULES)

Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ Wrong Format

File submitted was in the alphabetical heading format of the Old Sequence Rules.This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98

1645

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/956,518*

DATE: 01/21/99
TIME: 15:21:10

INPUT SET: S30866.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Corrected Diskette Needed
Does Not Comply

```
 1                                SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5      (i) APPLICANT: Leonard, Sherry
 6                    Freedman, Robert
 7
 8     (ii) TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR
 9
10    (iii) NUMBER OF SEQUENCES: 121
11
12     (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: MEDLEN & CARROLL, LLP
14           (B) STREET: 220 Montgomery Street, Suite 2200
15           (C) CITY: San Francisco
16           (D) STATE: CA
17           (E) COUNTRY: USA
18           (F) ZIP: 94104
19
20      (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26     (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: US 08/956,518
28           (B) FILING DATE: 23-OCT-1997
29           (C) CLASSIFICATION:
30
31   (viii) ATTORNEY/AGENT INFORMATION:
32           (A) NAME: MacKnight, Kamrin T.
33           (B) REGISTRATION NUMBER: 38,230
34           (C) REFERENCE/DOCKET NUMBER: UTC-03042
35
36     (ix) TELECOMMUNICATION INFORMATION:
37           (A) TELEPHONE: 415-705-8410
38           (B) TELEFAX: 415-397-8338
39
40
```

ERRORED SEQUENCES FOLLOW:

```
185    (2) INFORMATION FOR SEQ ID NO:9:
186
187         (i) SEQUENCE CHARACTERISTICS:
188             (A) LENGTH: 337 base pairs
189             (B) TYPE: nucleic acid
190             (C) STRANDEDNESS: single
191             (D) TOPOLOGY: linear
192
193         (ii) MOLECULE TYPE: other nucleic acid
194             (A) DESCRIPTION: /desc = "DNA"
195
196
197
198
199         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
200
201    AGATGCCCAA GTGGACCAGA GTCATCCTTC TGAACTGGTG CGCGTGGTTC
202    CTGCGAATGA        60
203
204    AGAGGCCCGG GGAGGACAAG GTGCGCCCGG CCTGCCAGCA CAAGCAGCGG
205    CGCTGCAGCC       120
206
207    TGGCCAGTGT GGAGATGAGC GCCGTGGGCC CGCCGCCCGC CAGCAACGGG
208    AACCTGCTGT       180
209
210    ACATCGGCTT CCGCGGCCTG GACGGCGTGC ACTGTGTCCC GACCCCCGAC
211    TCTGGGGTAG       240
212
213    TGTGTGGCCG CATGGCCTGC TCCCCCACGC ACGATGAGCA CCTCCTGCAC
214    GGCGGGCAAC       300
215
216    CCCCCGAGGG GGACCCGGAC TTGGCCAAGA TCCTGGA                      337
217
```

```
236    (2) INFORMATION FOR SEQ ID NO:11:
237
238         (i) SEQUENCE CHARACTERISTICS:
239             (A) LENGTH: 54 base pairs
240             (B) TYPE: nucleic acid
241             (C) STRANDEDNESS: single
242             (D) TOPOLOGY: linear
243
244         (ii) MOLECULE TYPE: other nucleic acid
245             (A) DESCRIPTION: /desc = "DNA"
246
247
248
249
250         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
251
252    CACACACACA TCACACACAC ACACACACAC ACACATACAC ACACACACCA CACA
253             54
254
```

```
921     (2) INFORMATION FOR SEQ ID NO:49:
922
923          (i) SEQUENCE CHARACTERISTICS:
924             (A) LENGTH: 48 base pairs
925             (B) TYPE: nucleic acid
926             (C) STRANDEDNESS: single
927             (D) TOPOLOGY: linear
928
929         (ii) MOLECULE TYPE: other nucleic acid
930             (A) DESCRIPTION: /desc = "DNA"
931
932
933
934
935         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
936
937     CAUCAUCAUC AUCCAGCGTA CATCGATGTA GCAGGAACTC TTGAATAT
938        48
939
```

same

```
940     (2) INFORMATION FOR SEQ ID NO:50:
941
942          (i) SEQUENCE CHARACTERISTICS:
943             (A) LENGTH: 41 base pairs
944             (B) TYPE: nucleic acid
945             (C) STRANDEDNESS: single
946             (D) TOPOLOGY: linear
947
948         (ii) MOLECULE TYPE: other nucleic acid
949             (A) DESCRIPTION: /desc = "DNA"
950
951
952         (ix) FEATURE:
953             (A) NAME/KEY: -
954             (B) LOCATION: 32..33
955             (D) OTHER INFORMATION: /note= "The residue at this
956     position is Inosine."
957
958         (ix) FEATURE:
959             (A) NAME/KEY: -
960             (B) LOCATION: 36..37
961             (D) OTHER INFORMATION: /note= "The residue at this
962     position is Inosine."
963
964         (ix) FEATURE:
965             (A) NAME/KEY: -
966             (B) LOCATION: 41..42?
967             (D) OTHER INFORMATION: /note= "The residue at this
968     position is Inosine."
969
970
971         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
```

"C" at location 32 can only represent itself, "G" at location 33 only represents itself. nothing else

If you want location 32 to be Inosine, use "N". Same with location 33

same error

42? There are only 41 nucleic acids in the sequence

same error

Inosine can only be represented by "N".

```
972
973     CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGCGGGG G                        41
974     41
975
```

```
1570    (2) INFORMATION FOR SEQ ID NO:84:
1571
1572         (i) SEQUENCE CHARACTERISTICS:
-->  1573             (A) LENGTH: 55 base pairs
1574             (B) TYPE: nucleic acid
1575             (C) STRANDEDNESS: single
1576             (D) TOPOLOGY: linear
1577
1578        (ii) MOLECULE TYPE: other nucleic acid
1579             (A) DESCRIPTION: /desc = "DNA"
1580
1581
1582
1583
1584        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
1585
1586    NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCT
-->  1587    GCACG              55
1588
```

```
1751    (2) INFORMATION FOR SEQ ID NO:94:
1752
1753         (i) SEQUENCE CHARACTERISTICS:
-->  1754             (A) LENGTH: 457 base pairs
1755             (B) TYPE: nucleic acid
1756             (C) STRANDEDNESS: single
1757             (D) TOPOLOGY: linear
1758
1759        (ii) MOLECULE TYPE: other nucleic acid
1760             (A) DESCRIPTION: /desc = "DNA"
1761
1762
1763
1764
1765        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
1766
1767    AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
-->  1768    CAGAGGCGCG         60
1769
1770    AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
-->  1771    ACCCAGCGCC        120
1772
1773    GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
-->  1774    GAGACGCTGG        180
1775
1776    CCCGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
-->  1777    TCACGTGGAG        240
1778
```

```
      1779   AGGCGCGCGG GGGCGGGCGG GGCGGGGGCG CGCGCCCGGC TCCTTAAAGG
-->   1780   CGCGCGAGCC       300
      1781
      1782   GAGCGGCGAG GTGCCTCTGT GGCCGCAGGC GCAGGCCCGG GCGACAGCCG
-->   1783   AGACGTGGAG       360
      1784
      1785   CGCGCCGGCT CGCTGCAGCT CCGGGACTCA ACATGCGCTG CTCGCCGGGA
-->   1786   GGCGTCTGGC       420
      1787
      1788   TGGCGCTGGC CGCGTCGCTC CTGCACGGTA AAGCCAC                   457
      1789
```

```
      1790   (2) INFORMATION FOR SEQ ID NO:95:
      1791
      1792          (i) SEQUENCE CHARACTERISTICS:
-->   1793              (A) LENGTH: 308 base pairs
      1794              (B) TYPE: nucleic acid
      1795              (C) STRANDEDNESS: single
      1796              (D) TOPOLOGY: linear
      1797
      1798         (ii) MOLECULE TYPE: other nucleic acid
      1799              (A) DESCRIPTION: /desc = "DNA"
      1800
      1801
      1802
      1803
      1804         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
      1805
      1806   CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCCT TGCCATTTTC
-->   1807   CAGCCGCGTC        60
      1808
      1809   CCACGAGGGT CACGGCGGCG GGGAGAGGTG GAGCCGCGAG AGCTCGGCCG
-->   1810   GGGGCCCCGC       120
      1811
      1812   CTGGTGGCCG CGGCCATGAC AGCGGCTCGG GACTGGCTCC TTTTCCGCGC
-->   1813   CCCTCCCGCC       180
      1814
      1815   GGAGGTGAGG GGAAGATGTC CATGTCAGGG TTCAAGGCCA AACCGAAGTT
-->   1816   ACTGGCCCTC       240
      1817
      1818   TATCTTCCAG GAGAACCAGG AGCCACAGCC GCGGCTCACG CCCCACCGCA
-->   1819   ACATTAAGGT       300
      1820
      1821   GAGTCGCC                                                  308
      1822
```

```
      1823   (2) INFORMATION FOR SEQ ID NO:96:
      1824
      1825          (i) SEQUENCE CHARACTERISTICS:
-->   1826              (A) LENGTH: 145 base pairs
      1827              (B) TYPE: nucleic acid
      1828              (C) STRANDEDNESS: single
      1829              (D) TOPOLOGY: linear
```

INPUT SET: S30866.raw

```
1830
1831        (ii) MOLECULE TYPE: other nucleic acid
1832              (A) DESCRIPTION: /desc = "DNA"
1833
1834
1835
1836
1837        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
1838
1839    CTCATTTCAG ATTACAAGTG GACACCTGAG TCAGCAGGAC CTGGAATCCC
--> 1840    AGATGAGAGA        60
1841
1842    GCTTATCTAC ACGACTCAGA TCTTGTTGTC ACCCCCATTA TTGACAATCC
--> 1843    AAAGGTGCAG        120
1844
1845    AAAGCACTCT GACAAGTGAG TTGTA                                      145
1846
```

```
1847    (2) INFORMATION FOR SEQ ID NO:97:
1848
1849        (i) SEQUENCE CHARACTERISTICS:
--> 1850            (A) LENGTH: 84 base pairs
1851            (B) TYPE: nucleic acid
1852            (C) STRANDEDNESS: single
1853            (D) TOPOLOGY: linear
1854
1855        (ii) MOLECULE TYPE: other nucleic acid
1856              (A) DESCRIPTION: /desc = "DNA"
1857
1858
1859
1860
1861        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
1862
1863    TTAACCACAG ATAATGAAAC AACCACCATC GGTTAAATTT GATGCAAAAA
--> 1864    TATTGCATCT        60
1865
1866    ACCAGCATTT TCAGGTAGGA TCAT                                       84
1867
```

```
1868    (2) INFORMATION FOR SEQ ID NO:98:
1869
1870        (i) SEQUENCE CHARACTERISTICS:
--> 1871            (A) LENGTH: 67 base pairs
1872            (B) TYPE: nucleic acid
1873            (C) STRANDEDNESS: single
1874            (D) TOPOLOGY: linear
1875
1876        (ii) MOLECULE TYPE: other nucleic acid
1877              (A) DESCRIPTION: /desc = "DNA"
1878
1879
1880
```

```
1881
1882          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
1883
1884     TTTATTCTAG TTCCAATTGC TAATCCAGCA TTTGTGGATA GCTGCAAACT
-->  1885     GCGATATGTA          60
1886
1887     AGTAACA                                                      67
1888
```

```
1889     (2) INFORMATION FOR SEQ ID NO:99:
1890
1891          (i) SEQUENCE CHARACTERISTICS:
-->  1892              (A) LENGTH: 100 base pairs
1893              (B) TYPE: nucleic acid
1894              (C) STRANDEDNESS: single
1895              (D) TOPOLOGY: linear
1896
1897          (ii) MOLECULE TYPE: other nucleic acid
1898              (A) DESCRIPTION: /desc = "DNA"
1899
1900
1901
1902
1903          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
1904
1905     CTGTTTCTAG TGCTGATGAG CGCTTTGACG CCACATTCCA CACTAACGTG
-->  1906     TTGGTGAATT          60
1907
1908     CTTCTGGGCA TTGCCAGTAC CTGCCTCCAG GTAAGCTGCA              100
1909
```

```
1928     (2) INFORMATION FOR SEQ ID NO:101:
1929
1930          (i) SEQUENCE CHARACTERISTICS:
-->  1931              (A) LENGTH: 392 base pairs
1932              (B) TYPE: nucleic acid
1933              (C) STRANDEDNESS: single
1934              (D) TOPOLOGY: linear
1935
1936          (ii) MOLECULE TYPE: other nucleic acid
1937              (A) DESCRIPTION: /desc = "DNA"
1938
1939
1940
1941
1942          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
1943
1944     AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
-->  1945     CAGAGGCGCG          60
1946
1947     AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
-->  1948     ACCCAGCGCC          120
1949
```

```
      1950   GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
-->   1951   GAGACGCTGG      180
      1952
      1953   CCCGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
-->   1954   TCACGTGGAG      240
      1955
      1956   AGGCGCGCGG GGGCGGGCGG GGCGGGGGCG CGCGCCCGGC TCCTTAAAGG
-->   1957   CGCGCGAGCC      300
      1958
      1959   GAGCGGCGAG GTGCCTCTGT GGCCGCAGGC GCAGGCCCGG GCGACAGCCG
-->   1960   AGACGTGGAG      360
      1961
      1962   CGCGCCGGCT CGCTGCAGCT CCGGGACTCA AC                        392
      1963
```

```
      1964   (2) INFORMATION FOR SEQ ID NO:102:
      1965
      1966       (i) SEQUENCE CHARACTERISTICS:
-->   1967           (A) LENGTH: 689 base pairs
      1968           (B) TYPE: nucleic acid
      1969           (C) STRANDEDNESS: single
      1970           (D) TOPOLOGY: linear
      1971
      1972      (ii) MOLECULE TYPE: other nucleic acid
      1973           (A) DESCRIPTION: /desc = "DNA"
      1974
      1975
      1976
      1977
      1978      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
      1979
      1980   AGCCCTTTCC CAGGCGGTAG CGGGGGCAGT GGTGCTGTTG CCCTTTTAAA
-->   1981   CTGCGGCTTG      60
      1982
      1983   ACGGGAGCCG CGCCTCCTGT CGGTGGAGTC GGTTATAAAG GGAGCAGCCC
-->   1984   CGCAGGCCGC      120
      1985
      1986   CACATAGCTC CCGCCAAGTC CTCGGTGCCC CTTGCCATTT TCCAGCCGCG
-->   1987   CTCCCACGAG      180
      1988
      1989   GGTCACGGCG GCGGGGAGAG GTGGAGCCGC GAGAGCTCGG CCGGGGGCCC
-->   1990   CGCCTGGTGG      240
      1991
      1992   CCGCGGCCAT GACAGCGGCT CGGGACTGGC TCCTTTTCCG CGCCCCTCCC
-->   1993   GCCGGAGGTG      300
      1994
      1995   AGGGGAAGAT GTCCATGTCA GGGTTCAAGG CCAAACCGAA GTTACTGGCC
-->   1996   TCTATCTTCC      360
      1997
      1998   AGGAGAACCA GGAGCCACAG CCGCGGCTCA CGCCCCACCG CAACATTAAG
-->   1999   ATTACAAGTG      420
      2000
      2001   GACACCTGAG TCAGCAGGAC CTGGAATCCC AGATGAGAGA GCTTATCTAC
```

INPUT SET: S30866.raw

--> 2002   ACGACTCAGA   480
    2003
    2004   TCTTGTTGTC ACCCCCATTA TTGACAATCC AAAGGTGCAG AAAGCACTCT
--> 2005   GACAATTCCA   540
    2006
    2007   ATTGCTAATC CAGCATTTGT GGATAGCTGC AAACTGCGAT ATTGCTGATG
--> 2008   AGCGCTTTGA   600
    2009
    2010   CGCCACATTC CACACTAACG TGTTGGTGAA TTCTTCTGGG CATTGCCAGT
--> 2011   ACCTGCCTCC   660
    2012
    2013   AGGCATATTC AAGAGTTCCT GCTACATCG   689
    2014

    2015   (2) INFORMATION FOR SEQ ID NO:103:
    2016
    2017   (i) SEQUENCE CHARACTERISTICS:
--> 2018   (A) LENGTH: 641 base pairs
    2019   (B) TYPE: nucleic acid
    2020   (C) STRANDEDNESS: single
    2021   (D) TOPOLOGY: linear
    2022
    2023   (ii) MOLECULE TYPE: other nucleic acid
    2024   (A) DESCRIPTION: /desc = "DNA"
    2025
    2026
    2027
    2028
    2029   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
    2030
    2031   CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCCT TGCCATTTTC
--> 2032   CAGCCGCGCT   60
    2033
    2034   CCCACGAGGG TCACGGCGGC GGGGAGAGGT GGAGCCGCGA GAGCTCGGCC
--> 2035   GGGGGCCCCG   120
    2036
    2037   CCTGGTGGCC GCGGCCATGA CAGCGGCTCG GGACTGGCTC CTTTTCCGCG
--> 2038   CCCCTCCCGC   180
    2039
    2040   CGGAGGTGAG GGGAAGATGT CCATGTCAGG GTTCAAGGCC AAACCGAAGT
--> 2041   TACTGGCCTC   240
    2042
    2043   TATCTTCCAG GAGAACCAGG AGCCACAGCC GCGGCTCACG CCCCACCGCA
--> 2044   ACATTAAGAT   300
    2045
    2046   TACAAGTGGA CACCTGAGTC AGCAGGACCT GGAATCCCAG ATGAGAGAGC
--> 2047   TTATCTACAC   360
    2048
    2049   GACTCAGATC TTGTTGTCAC CCCCATTATT GACAATCCAA AGGTGCAGAA
--> 2050   AGCACTCTGA   420
    2051
    2052   CAAATAATGA AACAACCACC ATCGGTTAAA TTTGATGCAA AAATATTGCA
--> 2053   TCTACCAGCA   480

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/956,518*

DATE: 01/21/99
TIME: 15:21:17

INPUT SET: S30866.raw

```
       2054
       2055     TTTTCAGTTC CAATTGCTAA TCCAGCATTT GTGGATAGCT GCAAACTGCG
-->    2056     ATATTGCTGA      540
       2057
       2058     TGAGCGCTTT GACGCCACAT TCCACACTAA CGTGTTGGTG AATTCTTCTG
-->    2059     GGCATTGCCA      600
       2060
       2061     GTACCTGCCT CCAGGCATAT TCAAGAGTTC CTGCTACATC G                641
       2062
```

```
       2081     (2) INFORMATION FOR SEQ ID NO:105:
       2082
       2083          (i) SEQUENCE CHARACTERISTICS:
-->    2084              (A) LENGTH: 140 base pairs
       2085              (B) TYPE: nucleic acid
       2086              (C) STRANDEDNESS: single
       2087              (D) TOPOLOGY: linear
       2088
       2089          (ii) MOLECULE TYPE: other nucleic acid
       2090              (A) DESCRIPTION: /desc = "DNA"
       2091
       2092
       2093
       2094
       2095          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
       2096
       2097     TGTCCNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->    2098     NNNNNNNNNN      60
       2099
       2100     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->    2101     NNNNNNNNNN      120
       2102
       2103     NNNNNNNNNN NNNNGACGTG                                      140
       2104
```

```
       2123     (2) INFORMATION FOR SEQ ID NO:107:
       2124
       2125          (i) SEQUENCE CHARACTERISTICS:
-->    2126              (A) LENGTH: 44 base pairs
       2127              (B) TYPE: nucleic acid
       2128              (C) STRANDEDNESS: single
       2129              (D) TOPOLOGY: linear
       2130
       2131          (ii) MOLECULE TYPE: other nucleic acid
       2132              (A) DESCRIPTION: /desc = "DNA"
       2133
       2134
       2135
       2136
       2137          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
       2138
       2139     GATGAGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCA AATG
       2140         44
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/956,518*

DATE: 01/21/99
TIME: 15:21:18

INPUT SET: S30866.raw

```
        2141
```

```
        2160   (2) INFORMATION FOR SEQ ID NO:109:
        2161
        2162        (i) SEQUENCE CHARACTERISTICS:
-->     2163            (A) LENGTH: 110 base pairs
        2164            (B) TYPE: nucleic acid
        2165            (C) STRANDEDNESS: single
        2166            (D) TOPOLOGY: linear
        2167
        2168       (ii) MOLECULE TYPE: other nucleic acid
        2169            (A) DESCRIPTION: /desc = "DNA"
        2170
        2171
        2172
        2173
        2174       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
        2175
        2176   TCTTGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->     2177   NNNNNNNNNN        60
        2178
        2179   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNAACAG
        2180            110
        2181
```

same

```
        2200   (2) INFORMATION FOR SEQ ID NO:111:
        2201
        2202        (i) SEQUENCE CHARACTERISTICS:
-->     2203            (A) LENGTH: 80 base pairs
        2204            (B) TYPE: nucleic acid
        2205            (C) STRANDEDNESS: single
        2206            (D) TOPOLOGY: linear
        2207
        2208       (ii) MOLECULE TYPE: other nucleic acid
        2209            (A) DESCRIPTION: /desc = "DNA"
        2210
        2211
        2212
        2213
        2214       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
        2215
        2216   GCTGATNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->     2217   NNNNNNNNNN        60
        2218
        2219   NNNNNNNNNN NNNCCTCCAG                                      80
        2220
```

same

```
        2239   (2) INFORMATION FOR SEQ ID NO:113:
        2240
        2241        (i) SEQUENCE CHARACTERISTICS:
-->     2242            (A) LENGTH: 168 base pairs
        2243            (B) TYPE: nucleic acid
        2244            (C) STRANDEDNESS: single
```

```
      2245           (D) TOPOLOGY: linear
      2246
      2247       (ii) MOLECULE TYPE: other nucleic acid
      2248           (A) DESCRIPTION: /desc = "DNA"
      2249
      2250
      2251
      2252
      2253       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
      2254
      2255   GCATANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->   2256   NNNNNNNNNN        60
      2257
      2258   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->   2259   NNNNNNNNNN       120
      2260
      2261   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NCTAGTGG
      2262          168
      2263
```

```
      2282   (2) INFORMATION FOR SEQ ID NO:115:
      2283
      2284       (i) SEQUENCE CHARACTERISTICS:
-->   2285           (A) LENGTH: 195 base pairs
      2286           (B) TYPE: nucleic acid
      2287           (C) STRANDEDNESS: single
      2288           (D) TOPOLOGY: linear
      2289
      2290       (ii) MOLECULE TYPE: other nucleic acid
      2291           (A) DESCRIPTION: /desc = "DNA"
      2292
      2293
      2294
      2295
      2296       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
      2297
      2298   GAATCNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->   2299   NNNNNNNNNN        60
      2300
      2301   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->   2302   NNNNNNNNNN       120
      2303
      2304   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->   2305   NNNNNNNNNN       180
      2306
      2307   NNNNNNNNTC CCTGG                                        195
      2308
```

```
      2327   (2) INFORMATION FOR SEQ ID NO:117:
      2328
      2329       (i) SEQUENCE CHARACTERISTICS:
-->   2330           (A) LENGTH: 87 base pairs
      2331           (B) TYPE: nucleic acid
```

INPUT SET: S30866.raw

```
2332              (C) STRANDEDNESS: single
2333              (D) TOPOLOGY: linear
2334
2335         (ii) MOLECULE TYPE: other nucleic acid
2336              (A) DESCRIPTION: /desc = "DNA"
2337
2338
2339
2340
2341         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
2342
2343    GGATANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
2344    NNNNNNNNNN         60
2345
2346    NNNNNNNNNN NNNNNNNNNN TTGATAG                                    87
2347
```

```
2366    (2)  INFORMATION FOR SEQ ID NO:119:
2367
2368         (i) SEQUENCE CHARACTERISTICS:
2369             (A) LENGTH: 110 base pairs
2370             (B) TYPE: nucleic acid
2371             (C) STRANDEDNESS: single
2372             (D) TOPOLOGY: linear
2373
2374         (ii) MOLECULE TYPE: other nucleic acid
2375              (A) DESCRIPTION: /desc = "DNA"
2376
2377
2378
2379
2380         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
2381
2382    CCCAGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
2383    NNNNNNNNNN         60
2384
2385    NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNAAGTGG
2386              110
2387
```

```
2406    (2)  INFORMATION FOR SEQ ID NO:121:
2407
2408         (i) SEQUENCE CHARACTERISTICS:
2409             (A) LENGTH: 519 base pairs
2410             (B) TYPE: nucleic acid
2411             (C) STRANDEDNESS: single
2412             (D) TOPOLOGY: linear
2413
2414         (ii) MOLECULE TYPE: other nucleic acid
2415              (A) DESCRIPTION: /desc = "DNA"
2416
2417
2418
```

```
2419
2420        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
2421
2422     ACCAGANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2423     NNNNNNNNNN         60
2424
2425     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2426     NNNNNNNNNN        120
2427
2428     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2429     NNNNNNNNNN        180
2430
2431     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2432     NNNNNNNNNN        240
2433
2434     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2435     NNNNNNNNNN        300
2436
2437     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2438     NNNNNNNNNN        360
2439
2440     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2441     NNNNNNNNNN        420
2442
2443     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
-->  2444     NNNNNNNNNN        480
2445
2446     NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNN
2447     519
2448
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/956,518*

INPUT SET: S30866.raw

Line	Error	Original Text
188	Entered (337) and Calc. Seq. Length (87) differ	(A) LENGTH: 337 base pairs
202	# of Sequences for line conflicts w/ running total	CTGCGAATGA 60
205	# of Sequences for line conflicts w/ running total	CGCTGCAGCC 120
208	# of Sequences for line conflicts w/ running total	AACCTGCTGT 180
211	# of Sequences for line conflicts w/ running total	TCTGGGGTAG 240
214	# of Sequences for line conflicts w/ running total	GGCGGGCAAC 300
239	Entered (54) and Calc. Seq. Length (0) differ	(A) LENGTH: 54 base pairs
924	Entered (48) and Calc. Seq. Length (0) differ	(A) LENGTH: 48 base pairs
943	Entered (41) and Calc. Seq. Length (0) differ	(A) LENGTH: 41 base pairs
1573	Entered (55) and Calc. Seq. Length (5) differ	(A) LENGTH: 55 base pairs
1587	# of Sequences for line conflicts w/ running total	GCACG 55
1754	Entered (457) and Calc. Seq. Length (107) differ	(A) LENGTH: 457 base pairs
1768	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1771	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1774	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1777	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1780	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1783	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1786	# of Sequences for line conflicts w/ running total	GGCGTCTGGC 420
1793	Entered (308) and Calc. Seq. Length (58) differ	(A) LENGTH: 308 base pairs
1807	# of Sequences for line conflicts w/ running total	CAGCCGCGTC 60
1810	# of Sequences for line conflicts w/ running total	GGGGCCCCGC 120
1813	# of Sequences for line conflicts w/ running total	CCCTCCCGCC 180
1816	# of Sequences for line conflicts w/ running total	ACTGGCCCTC 240
1819	# of Sequences for line conflicts w/ running total	ACATTAAGGT 300
1826	Entered (145) and Calc. Seq. Length (45) differ	(A) LENGTH: 145 base pairs
1840	# of Sequences for line conflicts w/ running total	AGATGAGAGA 60
1843	# of Sequences for line conflicts w/ running total	AAAGGTGCAG 120
1850	Entered (84) and Calc. Seq. Length (34) differ	(A) LENGTH: 84 base pairs
1864	# of Sequences for line conflicts w/ running total	TATTGCATCT 60
1871	Entered (67) and Calc. Seq. Length (17) differ	(A) LENGTH: 67 base pairs
1885	# of Sequences for line conflicts w/ running total	GCGATATGTA 60
1892	Entered (100) and Calc. Seq. Length (50) differ	(A) LENGTH: 100 base pairs
1906	# of Sequences for line conflicts w/ running total	TTGGTGAATT 60
1931	Entered (392) and Calc. Seq. Length (92) differ	(A) LENGTH: 392 base pairs
1945	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1948	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1951	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1954	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1957	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1960	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1967	Entered (689) and Calc. Seq. Length (139) differ	(A) LENGTH: 689 base pairs
1981	# of Sequences for line conflicts w/ running total	CTGCGGCTTG 60
1984	# of Sequences for line conflicts w/ running total	CGCAGGCCGC 120
1987	# of Sequences for line conflicts w/ running total	CTCCCACGAG 180
1990	# of Sequences for line conflicts w/ running total	CGCCTGGTGG 240
1993	# of Sequences for line conflicts w/ running total	GCCGGAGGTG 300
1996	# of Sequences for line conflicts w/ running total	TCTATCTTCC 360

# SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/956,518*

INPUT SET: S30866.raw

Line	Error	Original Text	
1999	# of Sequences for line conflicts w/ running total	ATTACAAGTG	420
2002	# of Sequences for line conflicts w/ running total	ACGACTCAGA	480
2005	# of Sequences for line conflicts w/ running total	GACAATTCCA	540
2008	# of Sequences for line conflicts w/ running total	AGCGCTTTGA	600
2011	# of Sequences for line conflicts w/ running total	ACCTGCCTCC	660
2018	Entered (641) and Calc. Seq. Length (141) differ	(A) LENGTH: 641 base pairs	
2032	# of Sequences for line conflicts w/ running total	CAGCCGCGCT	60
2035	# of Sequences for line conflicts w/ running total	GGGGGCCCCG	120
2038	# of Sequences for line conflicts w/ running total	CCCCTCCCGC	180
2041	# of Sequences for line conflicts w/ running total	TACTGGCCTC	240
2044	# of Sequences for line conflicts w/ running total	ACATTAAGAT	300
2047	# of Sequences for line conflicts w/ running total	TTATCTACAC	360
2050	# of Sequences for line conflicts w/ running total	AGCACTCTGA	420
2053	# of Sequences for line conflicts w/ running total	TCTACCAGCA	480
2056	# of Sequences for line conflicts w/ running total	ATATTGCTGA	540
2059	# of Sequences for line conflicts w/ running total	GGCATTGCCA	600
2084	Entered (140) and Calc. Seq. Length (40) differ	(A) LENGTH: 140 base pairs	
2098	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2101	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	120
2126	Entered (44) and Calc. Seq. Length (0) differ	(A) LENGTH: 44 base pairs	
2163	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs	
2177	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2203	Entered (80) and Calc. Seq. Length (30) differ	(A) LENGTH: 80 base pairs	
2217	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2242	Entered (168) and Calc. Seq. Length (20) differ	(A) LENGTH: 168 base pairs	
2256	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2259	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	120
2285	Entered (195) and Calc. Seq. Length (45) differ	(A) LENGTH: 195 base pairs	
2299	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2302	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	120
2305	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	180
2330	Entered (87) and Calc. Seq. Length (37) differ	(A) LENGTH: 87 base pairs	
2344	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2369	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs	
2383	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2409	Entered (519) and Calc. Seq. Length (80) differ	(A) LENGTH: 519 base pairs	
2423	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	60
2426	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	120
2429	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	180
2432	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	240
2435	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	300
2438	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	360
2441	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	420
2444	# of Sequences for line conflicts w/ running total	NNNNNNNNNN	480
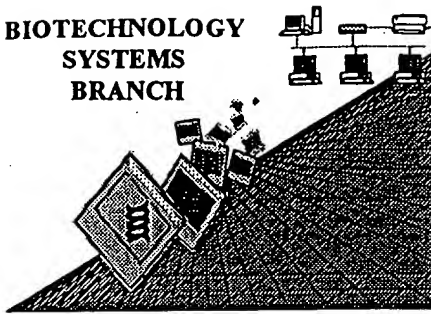
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   The software is in current directory: pub/checker/
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